

SEQUENCE DATA**TABLE 2: Sequences listed in this Disclosure**

SEQ. ID NO:	Designation	Reference
1	Lambda clone designated λ G ϕ 5 (ATCC Accession No. 98505) Contains human Telomerase Reverse Transcriptase (hTERT) genomic insert (residues 44-15375). The ATG translation initiation site begins at residue 13545.	GenBank Accession AF121948 International Patent Publication WO 00/46355.
2 – 5	Probes and Primers	(Artificial Sequences)
6	Sheep α 1,3-galactosyltransferase cDNA sequence	John Clark & Chris Denning; Geron Biomed
7	Sheep α 1,3-galactosyltransferase amino acid sequence	(<i>supra</i>)
8	Marmoset α 1,3-galactosyltransferase cDNA sequence	GenBank Accession S71333 See also Henion et al., Glycobiology 4,193 (1994)
9	Marmoset α 1,3-galactosyltransferase amino acid sequence	(<i>supra</i>)
10	Human histo blood group A transferase cDNA sequence	GenBank Accession J05175 See also Accession Nos. AF134413 & AF134412; Yamamoto et al., Nature 1990 May 17;345:229 (1990); U.S. Patent 5,326,857
11	Human histo blood group A transferase amino acid sequence	(<i>supra</i>)
12	Human histo blood group B transferase cDNA sequence	GenBank Accession AF134414 See also Yamamoto et al., Nature 1990 May 17;345:229 (1990); U.S. Patent 5,326,857
13	Human histo blood group B transferase amino acid sequence	(<i>supra</i>)
14-16	Probes and Primers	(Artificial Sequences)
17-20	Prototype α 1,3-galactosyltransferase catalytic domain/cytoplasmic domain fusions	This invention (Example 12)

SEQ. ID NO:1

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SEQUENCE LISTING

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McWhir, Jim
Gold, Joseph D.
Schiff, J. Michael

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<212> DNA
<213> Artificial

<400> 5

ggatgaagcg gagtctgga	19
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<210> 6
<211> 1303
<212> DNA
<213> Ovis aries

<220>
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cagatcagga gtcagaacgc tgcaccttcg cttcctccca gccctgcctc cttctgcaaa	120
acggagctca atagaacttg gtacttttgc cttttactct gggaggagag aagcagacga	180
tgaggagaaa ata atg aat gtc aaa gga aaa gtc att ctg tca atg ctg	229
Met Asn Val Lys Gly Lys Val Ile Leu Ser Met Leu	
1 5 10	
ggt gtc tca act gtc att gtt gtg ttt tgg gaa tat atc cac agc cca	277
Val Val Ser Thr Val Ile Val Val Phe Trp Glu Tyr Ile His Ser Pro	
15 20 25	
gaa ggc tct ttg ttc tgg ata aac cca tca aga aac cca gaa gtc agt	325
Glu Gly Ser Leu Phe Trp Ile Asn Pro Ser Arg Asn Pro Glu Val Ser	
30 35 40	
ggc ggc agc agc att cag aag ggc tgg tgg ttt ccg aga tgg ttt aac	373
Gly Gly Ser Ser Ile Gln Lys Gly Trp Trp Phe Pro Arg Trp Phe Asn	
45 50 55 60	
aat ggt tac caa gaa gaa gat gaa gac gta gac gaa gaa aag gaa caa	421
Asn Gly Tyr Gln Glu Glu Asp Glu Asp Val Asp Glu Glu Lys Glu Gln	
65 70 75	
aga aag gaa gac aaa agc aag ctt aag cta tcg gac tgg ttc aac cca	469
Arg Lys Glu Asp Lys Ser Lys Leu Lys Leu Ser Asp Trp Phe Asn Pro	
80 85 90	
ttt aaa cgc cct gag gtt gtg act atg aca gat tgg aag gca ccc gtg	517
Phe Lys Arg Pro Glu Val Val Thr Met Thr Asp Trp Lys Ala Pro Val	
95 100 105	
gtg tgg gaa ggc act tac aac aga gcc gtc tta gac gat tac tac gcc	565
Val Trp Glu Gly Thr Tyr Asn Arg Ala Val Leu Asp Asp Tyr Tyr Ala	
110 115 120	
aag cag aaa att acc gtc ggc ctg acg gtt ttc gcc gtc gga aga tac	613
Lys Gln Lys Ile Thr Val Gly Leu Thr Val Phe Ala Val Gly Arg Tyr	
125 130 135 140	
att gag cat tac ttg gag gag ttc tta acg tct gct aat aag cac ttc	661
Ile Glu His Tyr Leu Glu Glu Phe Leu Thr Ser Ala Asn Lys His Phe	
145 150 155	
atg gtt ggc cac cga gtc atc ttt tac gtc atg gtg gac gac gtc tcc	709
Met Val Gly His Arg Val Ile Phe Tyr Val Met Val Asp Asp Val Ser	
160 165 170	
agg atg cct ttg ata gag ctg ggc cct ctg cgc tcc ttc aaa gtg ttt	757
Arg Met Pro Leu Ile Glu Leu Gly Pro Leu Arg Ser Phe Lys Val Phe	
175 180 185	
gag gtc aag cct gag agg agg tgg cag gac gtc agc atg gtg cgc atg	805
Glu Val Lys Pro Glu Arg Arg Trp Gln Asp Val Ser Met Val Arg Met	
190 195 200	
aag acc atc ggg gag cac atc gtg gcc cac atc cag cgt gag gtt gac	853
Lys Thr Ile Gly Glu His Ile Val Ala His Ile Gln Arg Glu Val Asp	
205 210 215 220	
ttc ctc ttc tgc atg gac gtg gac cag gtc ttc caa gac gag ttc ggg	901
Phe Leu Phe Cys Met Asp Val Asp Gln Val Phe Gln Asp Glu Phe Gly	
225 230 235	
gtg gag acc ctg ggt gag tcg gtg gcc cag cta cag gcc tgg tgg tac	949
Val Glu Thr Leu Gly Glu Ser Val Ala Gln Leu Gln Ala Trp Trp Tyr	
240 245 250	
aag gca gat ccc gat gag ttt acc tac gag agg cgc aag gag tct gca	997
Lys Ala Asp Pro Asp Glu Phe Thr Tyr Glu Arg Arg Lys Glu Ser Ala	
255 260 265	
gca tac att ccc ttc ggc gaa ggg gat ttt tat tac cac gca gcc att	1045
Ala Tyr Ile Pro Phe Gly Glu Gly Asp Phe Tyr Tyr His Ala Ala Ile	
270 275 280	
ttt ggg gga aca ccc act cag gtc ctt aac atc acc cag gaa tgc ttc	1093
Phe Gly Gly Thr Pro Thr Gln Val Leu Asn Ile Thr Gln Glu Cys Phe	
285 290 295 300	
aaa gga atc ctc aag gac aag aaa aat gac ata gaa gcc caa tgg cat	1141
Lys Gly Ile Leu Lys Asp Lys Lys Asn Asp Ile Glu Ala Gln Trp His	
305 310 315	
gat gag agc cat cta aac aag tat ttc ctt ctc aac aaa ccc act aaa	1189
Asp Glu Ser His Leu Asn Lys Tyr Phe Leu Leu Asn Lys Pro Thr Lys	
320 325 330	
atc tta tcc ccg gaa tac tgc tgg gat tat cat ata ggc cta cct gcg	1237
Ile Leu Ser Pro Glu Tyr Cys Trp Asp Tyr His Ile Gly Leu Pro Ala	

335 340 345
gat att aag ctt gtc aag atg tct tgg cag aca aaa gag tat aat gtg 1285
Asp Ile Lys Leu Val Lys Met Ser Trp Gln Thr Lys Glu Tyr Asn Val
350 355 360
gtt aga aat aac gtc tga 1303
Val Arg Asn Asn Val
365

<210> 7
<211> 369
<212> PRT
<213> Ovis aries

<400> 7

Met Asn Val Lys Gly Lys Val Ile Leu Ser Met Leu Val Val Ser Thr
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Val Ile Val Val Phe Trp Glu Tyr Ile His Ser Pro Glu Gly Ser Leu
20 25 30
Phe Trp Ile Asn Pro Ser Arg Asn Pro Glu Val Ser Gly Gly Ser Ser
35 40 45
Ile Gln Lys Gly Trp Trp Phe Pro Arg Trp Phe Asn Asn Gly Tyr Gln
50 55 60
Glu Glu Asp Glu Asp Val Asp Glu Glu Lys Glu Gln Arg Lys Glu Asp
65 70 75 80
Lys Ser Lys Leu Lys Leu Ser Asp Trp Phe Asn Pro Phe Lys Arg Pro
85 90 95
Glu Val Val Thr Met Thr Asp Trp Lys Ala Pro Val Val Trp Glu Gly
100 105 110
Thr Tyr Asn Arg Ala Val Leu Asp Asp Tyr Tyr Ala Lys Gln Lys Ile
115 120 125
Thr Val Gly Leu Thr Val Phe Ala Val Gly Arg Tyr Ile Glu His Tyr
130 135 140
Leu Glu Glu Phe Leu Thr Ser Ala Asn Lys His Phe Met Val Gly His
145 150 155 160
Arg Val Ile Phe Tyr Val Met Val Asp Asp Val Ser Arg Met Pro Leu
165 170 175
Ile Glu Leu Gly Pro Leu Arg Ser Phe Lys Val Phe Glu Val Lys Pro
180 185 190
Glu Arg Arg Trp Gln Asp Val Ser Met Val Arg Met Lys Thr Ile Gly
195 200 205
Glu His Ile Val Ala His Ile Gln Arg Glu Val Asp Phe Leu Phe Cys
210 215 220
Met Asp Val Asp Gln Val Phe Gln Asp Glu Phe Gly Val Glu Thr Leu
225 230 235 240
Gly Glu Ser Val Ala Gln Leu Gln Ala Trp Trp Tyr Lys Ala Asp Pro
245 250 255
Asp Glu Phe Thr Tyr Glu Arg Arg Lys Glu Ser Ala Ala Tyr Ile Pro
260 265 270

Phe Gly Glu Gly Asp Phe Tyr Tyr His Ala Ala Ile Phe Gly Gly Thr
275 280 285

Pro Thr Gln Val Leu Asn Ile Thr Gln Glu Cys Phe Lys Gly Ile Leu
290 295 300

Lys Asp Lys Lys Asn Asp Ile Glu Ala Gln Trp His Asp Glu Ser His
305 310 315 320

Leu Asn Lys Tyr Phe Leu Leu Asn Lys Pro Thr Lys Ile Leu Ser Pro
325 330 335

Glu Tyr Cys Trp Asp Tyr His Ile Gly Leu Pro Ala Asp Ile Lys Leu
340 345 350

Val Lys Met Ser Trp Gln Thr Lys Glu Tyr Asn Val Val Arg Asn Asn
355 360 365

Val

<210> 8
<211> 1131
<212> DNA
<213> *Platyrrhinus helleri*

<220>
<221> CDS
<222> (1)..(1131)
<223>
<400> 8

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gtg att gtt gtg ttt tgg gaa tat atc aac agc cca gaa ggc tct ttc	96
Val Ile Val Val Phe Trp Glu Tyr Ile Asn Ser Pro Glu Gly Ser Phe	
20 25 30	
ttg tgg ata tat cac tca aag aac cca gaa gtt gat gac agc agt gct	144
Leu Trp Ile Tyr His Ser Lys Asn Pro Glu Val Asp Asp Ser Ser Ala	
35 40 45	
cag aag gac tgg tgg ttt cct ggc tgg ttt aac aat ggg atc cac aat	192
Gln Lys Asp Trp Trp Phe Pro Gly Trp Phe Asn Asn Gly Ile His Asn	
50 55 60	
tat caa caa gag gaa gaa gac aca gac aaa gaa aaa gga aga gag gag	240
Tyr Gln Gln Glu Glu Glu Asp Thr Asp Lys Glu Lys Gly Arg Glu Glu	
65 70 75 80	
gaa caa aaa aag gaa gat gac aca aca gag ctt cgg cta tgg gac tgg	288
Glu Gln Lys Lys Glu Asp Asp Thr Thr Glu Leu Arg Leu Trp Asp Trp	
85 90 95	
ttt aat cca aag aaa cgc cca gag gtt atg aca gtg acc caa tgg aag	336
Phe Asn Pro Lys Lys Arg Pro Glu Val Met Thr Val Thr Gln Trp Lys	
100 105 110	
gcg ccg gtt gtg tgg gaa ggc act tac aac aaa gcc atc cta gaa aat	384
Ala Pro Val Val Trp Glu Gly Thr Tyr Asn Lys Ala Ile Leu Glu Asn	
115 120 125	
tat tat gcc aaa cag aaa att acc gtg ggg ttg acg gtt ttt gct att	432
Tyr Tyr Ala Lys Gln Lys Ile Thr Val Gly Leu Thr Val Phe Ala Ile	
130 135 140	
gga aga tat att gag cat tac ttg gag gag ttc gta aca tct gct aat	480
Gly Arg Tyr Ile Glu His Tyr Leu Glu Glu Phe Val Thr Ser Ala Asn	
145 150 155 160	
agg tac ttc atg gtc ggc cac aaa gtc ata ttt tat gtc atg gtg gat	528
Arg Tyr Phe Met Val Gly His Lys Val Ile Phe Tyr Val Met Val Asp	
165 170 175	
gat gtc tcc aag gcg ccg ttt ata gag ctg ggt cct ctg cgt tcc ttc	576
Asp Val Ser Lys Ala Pro Phe Ile Glu Leu Gly Pro Leu Arg Ser Phe	

180	185	190	
aaa gtg ttt gag gtc aag cca gag aag agg tgg caa gac atc agc atg			624
Lys Val Phe Glu Val Lys Pro Glu Lys Arg Trp Gln Asp Ile Ser Met			
195	200	205	
atg cgt atg aag acc atc ggg gag cac atc ttg gcc cac atc caa cac			672
Met Arg Met Lys Thr Ile Gly Glu His Ile Leu Ala His Ile Gln His			
210	215	220	
gag gtt gac ttc ctc ttc tgc atg gat gtg gac cag gtc ttc caa gac			720
Glu Val Asp Phe Leu Phe Cys Met Asp Val Asp Gln Val Phe Gln Asp			
225	230	235	240
cat ttt ggg gta gag acc ctg ggc cag tcg gtg gct cag cta cag gcc			768
His Phe Gly Val Glu Thr Leu Gly Gln Ser Val Ala Gln Leu Gln Ala			
245	250	255	
tgg tgg tac aag gca gat cct gat gac ttt acc tat gag agg cgg aaa			816
Trp Trp Tyr Lys Ala Asp Pro Asp Asp Phe Thr Tyr Glu Arg Arg Lys			
260	265	270	
gag tcg gca gca tat att cca ttt ggc cag ggg gat ttt tat tac cat			864
Glu Ser Ala Ala Tyr Ile Pro Phe Gly Gln Gly Asp Phe Tyr Tyr His			
275	280	285	
gca gcc att ttt gga gga aca ccg att cag gtt ctc aac atc acc cag			912
Ala Ala Ile Phe Gly Gly Thr Pro Ile Gln Val Leu Asn Ile Thr Gln			
290	295	300	
gag tgc ttt aag gga atc ctc ctg gac aag aaa aat gac ata gaa gcc			960
Glu Cys Phe Lys Gly Ile Leu Leu Asp Lys Lys Asn Asp Ile Glu Ala			
305	310	315	320
gag tgg cat gat gaa agc cac cta aac aag tat ttc ctt ctc aac aaa			1008
Glu Trp His Asp Glu Ser His Leu Asn Lys Tyr Phe Leu Leu Asn Lys			
325	330	335	
ccc tct aaa atc tta tct cca gaa tac tgc tgg gat tat cat ata ggc			1056
Pro Ser Lys Ile Leu Ser Pro Glu Tyr Cys Trp Asp Tyr His Ile Gly			
340	345	350	
ctg cct tca gat att aaa act gtc aag cta tca tgg caa aca aaa gag			1104
Leu Pro Ser Asp Ile Lys Thr Val Lys Leu Ser Trp Gln Thr Lys Glu			
355	360	365	
tat aat ttg gtt aga aag aat gtc tga			1131
Tyr Asn Leu Val Arg Lys Asn Val			
370	375		

<210> 9
<211> 376
<212> PRT
<213> *Platyrrhinus helleri*

<400> 9

Met Asn Val Lys Gly Lys Val Ile Leu Ser Met Leu Val Val Ser Thr	
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Val Ile Val Val Phe Trp Glu Tyr Ile Asn Ser Pro Glu Gly Ser Phe	
20	30
Leu Trp Ile Tyr His Ser Lys Asn Pro Glu Val Asp Asp Ser Ser Ala	
35	45
Gln Lys Asp Trp Trp Phe Pro Gly Trp Phe Asn Asn Gly Ile His Asn	
50	60
Tyr Gln Gln Glu Glu Glu Asp Thr Asp Lys Glu Lys Gly Arg Glu Glu	
65	80
Glu Gln Lys Lys Glu Asp Asp Thr Thr Glu Leu Arg Leu Trp Asp Trp	
85	95
Phe Asn Pro Lys Lys Arg Pro Glu Val Met Thr Val Thr Gln Trp Lys	
100	110

Ala Pro Val Val Trp Glu Gly Thr Tyr Asn Lys Ala Ile Leu Glu Asn
115 120 125

Tyr Tyr Ala Lys Gln Lys Ile Thr Val Gly Leu Thr Val Phe Ala Ile
130 135 140

Gly Arg Tyr Ile Glu His Tyr Leu Glu Glu Phe Val Thr Ser Ala Asn
145 150 155 160

Arg Tyr Phe Met Val Gly His Lys Val Ile Phe Tyr Val Met Val Asp
165 170 175

Asp Val Ser Lys Ala Pro Phe Ile Glu Leu Gly Pro Leu Arg Ser Phe
180 185 190

Lys Val Phe Glu Val Lys Pro Glu Lys Arg Trp Gln Asp Ile Ser Met
195 200 205

Met Arg Met Lys Thr Ile Gly Glu His Ile Leu Ala His Ile Gln His
210 215 220

Glu Val Asp Phe Leu Phe Cys Met Asp Val Asp Gln Val Phe Gln Asp
225 230 235 240

His Phe Gly Val Glu Thr Leu Gly Gln Ser Val Ala Gln Leu Gln Ala
245 250 255

Trp Trp Tyr Lys Ala Asp Pro Asp Asp Phe Thr Tyr Glu Arg Arg Lys
260 265 270

Glu Ser Ala Ala Tyr Ile Pro Phe Gly Gln Gly Asp Phe Tyr Tyr His
275 280 285

Ala Ala Ile Phe Gly Gly Thr Pro Ile Gln Val Leu Asn Ile Thr Gln
290 295 300

Glu Cys Phe Lys Gly Ile Leu Leu Asp Lys Lys Asn Asp Ile Glu Ala
305 310 315 320

Glu Trp His Asp Glu Ser His Leu Asn Lys Tyr Phe Leu Leu Asn Lys
325 330 335

Pro Ser Lys Ile Leu Ser Pro Glu Tyr Cys Trp Asp Tyr His Ile Gly
340 345 350

Leu Pro Ser Asp Ile Lys Thr Val Lys Leu Ser Trp Gln Thr Lys Glu
355 360 365

Tyr Asn Leu Val Arg Lys Asn Val
370 375

<210> 10
<211> 1062
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)..(1062)
<223>
<400> 10

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Met Ala Glu Val Leu Arg Thr Leu Ala Gly Lys Pro Lys Cys His Ala	
1 5 10 15	
ctt cga cct atg atc ctt ttc cta ata atg ctt gtc ttg gtc ttg ttt	96
Leu Arg Pro Met Ile Leu Phe Leu Ile Met Leu Val Leu Val Leu Phe	

20	25	30	
ggg tac ggc gtc cta agc ccc aga agt cta atg cca gga agc ctg gaa			144
Gly Tyr Gly Val Leu Ser Pro Arg Ser Leu Met Pro Gly Ser Leu Glu			
35	40	45	
cgg ggg ttc tgc atg gct gtt agg gaa cct gac cat ctg cag cgc gtc			192
Arg Gly Phe Cys Met Ala Val Arg Glu Pro Asp His Leu Gln Arg Val			
50	55	60	
tcg ttg cca agg atg gtc tac ccc cag cca aag gtg ctg aca ccg tgg			240
Ser Leu Pro Arg Met Val Tyr Pro Gln Pro Lys Val Leu Thr Pro Trp			
65	70	75	80
aag gat gtc ctc gtg gtg acc cct tgg ctg gct ccc att gtc tgg gag			288
Lys Asp Val Leu Val Val Thr Pro Trp Leu Ala Pro Ile Val Trp Glu			
85	90	95	
ggc aca ttc aac atc gac atc ctc aac gag cag ttc agg ctc cag aac			336
Gly Thr Phe Asn Ile Asp Ile Leu Asn Glu Gln Phe Arg Leu Gln Asn			
100	105	110	
acc acc att ggg tta act gtg ttt gcc atc aag aaa tac gtg gct ttc			384
Thr Thr Ile Gly Leu Thr Val Phe Ala Ile Lys Lys Tyr Val Ala Phe			
115	120	125	
ctg aag ctg ttc ctg gag acg gcg gag aag cac ttc atg gtg ggc cac			432
Leu Lys Leu Phe Leu Glu Thr Ala Glu Lys His Phe Met Val Gly His			
130	135	140	
cgt gtc cac tac tat gtc ttc acc gac cag ctg gcc gcg gtg ccc cgc			480
Arg Val His Tyr Tyr Val Phe Thr Asp Gln Leu Ala Ala Val Pro Arg			
145	150	155	160
gtg acg ctg ggg acc ggt cgg cag ctg tca gtg ctg gag gtg cgc gcc			528
Val Thr Leu Gly Thr Gly Arg Gln Leu Ser Val Leu Glu Val Arg Ala			
165	170	175	
tac aag cgc tgg cag gac gtg tcc atg cgc cgc atg gag atg atc agt			576
Tyr Lys Arg Trp Gln Asp Val Ser Met Arg Arg Met Glu Met Ile Ser			
180	185	190	
gac ttc tgc gag cgg cgc ttc ctc agc gag gtg gat tac ctg gtg tgc			624
Asp Phe Cys Glu Arg Arg Phe Leu Ser Glu Val Asp Tyr Leu Val Cys			
195	200	205	
gtg gac gtg gac atg gag ttc cgc gac cac gtg ggc gtg gag atc ctg			672
Val Asp Val Asp Met Glu Phe Arg Asp His Val Gly Val Glu Ile Leu			
210	215	220	
act ccg ctg ttc ggc acc ctg cac ccc ggc ttc tac gga agc agc cgg			720
Thr Pro Leu Phe Gly Thr Leu His Pro Gly Phe Tyr Gly Ser Ser Arg			
225	230	235	240
gag gcc ttc acc tac gag cgc cgg ccc cag tcc cag gcc tac atc ccc			768
Glu Ala Phe Thr Tyr Glu Arg Arg Pro Gln Ser Gln Ala Tyr Ile Pro			
245	250	255	
aag gac gag ggc gat ttc tac tac ctg ggg ggg ttc ttc ggg ggg tcg			816
Lys Asp Glu Gly Asp Phe Tyr Tyr Leu Gly Gly Phe Phe Gly Gly Ser			
260	265	270	
gtg caa gag gtg cag cgg ctc acc agg gcc tgc cac cag gcc atg atg			864
Val Gln Glu Val Gln Arg Leu Thr Arg Ala Cys His Gln Ala Met Met			
275	280	285	
gtc gac cag gcc aac ggc atc gag gcc gtg tgg cac gac gag agc cac			912
Val Asp Gln Ala Asn Gly Ile Glu Ala Val Trp His Asp Glu Ser His			
290	295	300	
ctg aac aag tac ctg ctg cgc cac aaa ccc acc aag gtg ctc tcc ccc			960
Leu Asn Lys Tyr Leu Leu Arg His Lys Pro Thr Lys Val Leu Ser Pro			
305	310	315	320
gag tac ttg tgg gac cag cag ctg ctg ggc tgg ccc gcc gtc ctg agg			1008
Glu Tyr Leu Trp Asp Gln Gln Leu Leu Gly Trp Pro Ala Val Leu Arg			
325	330	335	
aag ctg agg ttc act gcg gtg ccc aag aac cac cag gcg gtc cgg aac			1056
Lys Leu Arg Phe Thr Ala Val Pro Lys Asn His Gln Ala Val Arg Asn			
340	345	350	
ccg tga			1062
Pro			

<210> 11
<211> 353

<212> PRT
<213> Homo sapiens

<400> 11

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20     25     30
Gly Tyr Gly Val Leu Ser Pro Arg Ser Leu Met Pro Gly Ser Leu Glu
35     40     45
Arg Gly Phe Cys Met Ala Val Arg Glu Pro Asp His Leu Gln Arg Val
50     55     60
Ser Leu Pro Arg Met Val Tyr Pro Gln Pro Lys Val Leu Thr Pro Trp
65     70     75     80
Lys Asp Val Leu Val Val Thr Pro Trp Leu Ala Pro Ile Val Trp Glu
85     90     95
Gly Thr Phe Asn Ile Asp Ile Leu Asn Glu Gln Phe Arg Leu Gln Asn
100    105    110
Thr Thr Ile Gly Leu Thr Val Phe Ala Ile Lys Lys Tyr Val Ala Phe
115    120    125
Leu Lys Leu Phe Leu Glu Thr Ala Glu Lys His Phe Met Val Gly His
130    135    140
Arg Val His Tyr Tyr Val Phe Thr Asp Gln Leu Ala Ala Val Pro Arg
145    150    155    160
Val Thr Leu Gly Thr Gly Arg Gln Leu Ser Val Leu Glu Val Arg Ala
165    170    175
Tyr Lys Arg Trp Gln Asp Val Ser Met Arg Arg Met Glu Met Ile Ser
180    185    190
Asp Phe Cys Glu Arg Arg Phe Leu Ser Glu Val Asp Tyr Leu Val Cys
195    200    205
Val Asp Val Asp Met Glu Phe Arg Asp His Val Gly Val Glu Ile Leu
210    215    220
Thr Pro Leu Phe Gly Thr Leu His Pro Gly Phe Tyr Gly Ser Ser Arg
225    230    235    240
Glu Ala Phe Thr Tyr Glu Arg Arg Pro Gln Ser Gln Ala Tyr Ile Pro
245    250    255
Lys Asp Glu Gly Asp Phe Tyr Tyr Leu Gly Gly Phe Phe Gly Gly Ser
260    265    270
Val Gln Glu Val Gln Arg Leu Thr Arg Ala Cys His Gln Ala Met Met
275    280    285
Val Asp Gln Ala Asn Gly Ile Glu Ala Val Trp His Asp Glu Ser His
290    295    300
Leu Asn Lys Tyr Leu Leu Arg His Lys Pro Thr Lys Val Leu Ser Pro
305    310    315    320
Glu Tyr Leu Trp Asp Gln Gln Leu Leu Gly Trp Pro Ala Val Leu Arg
325    330    335

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Lys Leu Arg Phe Thr Ala Val Pro Lys Asn His Gln Ala Val Arg Asn
340 345 350

Pro

<210> 12
<211> 1065
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)..(1065)
<223>
<400> 12

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ctt cga cct atg atc ctt ttc cta ata atg ctt gtc ttg gtc ttg ttt	96
Leu Arg Pro Met Ile Leu Phe Leu Ile Met Leu Val Leu Val Leu Phe	
20 25 30	
ggt tac ggg gtc cta agc ccc aga agt cta atg cca gga agc ctg gaa	144
Gly Tyr Gly Val Leu Ser Pro Arg Ser Leu Met Pro Gly Ser Leu Glu	
35 40 45	
cgg ggg ttc tgc atg gct gtt agg gaa cct gac cat ctg cag cgc gtc	192
Arg Gly Phe Cys Met Ala Val Arg Glu Pro Asp His Leu Gln Arg Val	
50 55 60	
tcg ttg cca agg atg gtc tac ccc cag cca aag gtg ctg aca ccg tgt	240
Ser Leu Pro Arg Met Val Tyr Pro Gln Pro Lys Val Leu Thr Pro Cys	
65 70 75 80	
agg aag gat gtc ctc gtg gtg acc cct tgg ctg gct ccc att gtc tgg	288
Arg Lys Asp Val Leu Val Val Thr Pro Trp Leu Ala Pro Ile Val Trp	
85 90 95	
gag ggc acg ttc aac atc gac atc ctc aac gag cag ttc agg ctc cag	336
Glu Gly Thr Phe Asn Ile Asp Ile Leu Asn Glu Gln Phe Arg Leu Gln	
100 105 110	
aac acc acc att ggg tta act gtg ttt gcc atc aag aaa tac gtg gct	384
Asn Thr Thr Ile Gly Leu Thr Val Phe Ala Ile Lys Lys Tyr Val Ala	
115 120 125	
ttc ctg aag ctg ttc ctg gag acg gcg gag aag cac ttc atg gtg ggc	432
Phe Leu Lys Leu Phe Leu Glu Thr Ala Glu Lys His Phe Met Val Gly	
130 135 140	
cac cgt gtc cac tac tat gtc ttc acc gac cag ccg gcc gcg gtg ccc	480
His Arg Val His Tyr Tyr Val Phe Thr Asp Gln Pro Ala Ala Val Pro	
145 150 155 160	
cgc gtg acg ctg ggg acc ggt cgg cag ctg tca gtg ctg gag gtg ggc	528
Arg Val Thr Leu Gly Thr Gly Arg Gln Leu Ser Val Leu Glu Val Gly	
165 170 175	
gcc tac aag cgc tgg cag gac gtg tcc atg cgc cgc atg gag atg atc	576
Ala Tyr Lys Arg Trp Gln Asp Val Ser Met Arg Arg Met Glu Met Ile	
180 185 190	
agt gac ttc tgc gag cgg cgc ttc ctc agc gag gtg gat tac ctg gtg	624
Ser Asp Phe Cys Glu Arg Arg Phe Leu Ser Glu Val Asp Tyr Leu Val	
195 200 205	
tgc gtg gac gtg gac atg gag ttc cgc gac cat gtg ggc gtg gag atc	672
Cys Val Asp Val Asp Met Glu Phe Arg Asp His Val Gly Val Glu Ile	
210 215 220	
ctg act ccg ctg ttc ggc acc ctg cac ccc agc ttc tac gga agc agc	720
Leu Thr Pro Leu Phe Gly Thr Leu His Pro Ser Phe Tyr Gly Ser Ser	
225 230 235 240	
cgg gag gcc ttc acc tac gag cgc cgg ccc cag tcc cag gcc tac atc	768
Arg Glu Ala Phe Thr Tyr Glu Arg Arg Pro Gln Ser Gln Ala Tyr Ile	
245 250 255	
ccc aag gac gag ggc gat ttc tac tac atg ggg gcg ttc ttc ggg ggg	816

Pro	Lys	Asp	Glu	Gly	Asp	Phe	Tyr	Tyr	Met	Gly	Ala	Phe	Phe	Gly	Gly		
			260					265					270				
tcg	gtg	caa	gag	gtg	cag	cgg	ctc	acc	agg	gcc	tgc	cac	cag	gcc	atg		864
Ser	Val	Gln	Glu	Val	Gln	Arg	Leu	Thr	Arg	Ala	Cys	His	Gln	Ala	Met		
		275					280					285					
atg	gtc	gac	cag	gcc	aac	ggc	atc	gag	gcc	gtg	tgg	cac	gac	gag	agc		912
Met	Val	Asp	Gln	Ala	Asn	Gly	Ile	Glu	Ala	Val	Trp	His	Asp	Glu	Ser		
	290					295				300							
cac	ctg	aac	aag	tac	cta	ctg	cgc	cac	aaa	ccc	acc	aag	gtg	ctc	tcc		960
His	Leu	Asn	Lys	Tyr	Leu	Leu	Arg	His	Lys	Pro	Thr	Lys	Val	Leu	Ser		
305					310					315					320		
ccc	gag	tac	ttg	tgg	gac	cag	cag	ctg	ctg	ggc	tgg	ccc	gcc	gtc	ctg		1008
Pro	Glu	Tyr	Leu	Trp	Asp	Gln	Gln	Leu	Gly	Trp	Pro	Ala	Val	Leu			
			325						330				335				
agg	aag	ctg	agg	ttc	act	gcg	gtg	ccc	aag	aac	cac	cag	gcg	gtc	cgg		1056
Arg	Lys	Leu	Arg	Phe	Thr	Ala	Val	Pro	Lys	Asn	His	Gln	Ala	Val	Arg		
			340					345					350				
aac	ccg	tga															1065
Asn	Pro																

<210> 13
<211> 354
<212> PRT
<213> Homo sapiens

<400> 13

Met	Ala	Glu	Val	Leu	Arg	Thr	Leu	Ala	Gly	Lys	Pro	Lys	Cys	His	Ala		
1				5					10					15			
Leu	Arg	Pro	Met	Ile	Leu	Phe	Leu	Ile	Met	Leu	Val	Leu	Val	Leu	Phe		
			20					25					30				
Gly	Tyr	Gly	Val	Leu	Ser	Pro	Arg	Ser	Leu	Met	Pro	Gly	Ser	Leu	Glu		
		35					40					45					
Arg	Gly	Phe	Cys	Met	Ala	Val	Arg	Glu	Pro	Asp	His	Leu	Gln	Arg	Val		
	50					55					60						
Ser	Leu	Pro	Arg	Met	Val	Tyr	Pro	Gln	Pro	Lys	Val	Leu	Thr	Pro	Cys		
65				70						75					80		
Arg	Lys	Asp	Val	Leu	Val	Val	Thr	Pro	Trp	Leu	Ala	Pro	Ile	Val	Trp		
			85						90					95			
Glu	Gly	Thr	Phe	Asn	Ile	Asp	Ile	Leu	Asn	Glu	Gln	Phe	Arg	Leu	Gln		
		100					105						110				
Asn	Thr	Thr	Ile	Gly	Leu	Thr	Val	Phe	Ala	Ile	Lys	Lys	Tyr	Val	Ala		
		115					120					125					
Phe	Leu	Lys	Leu	Phe	Leu	Glu	Thr	Ala	Glu	Lys	His	Phe	Met	Val	Gly		
	130					135					140						
His	Arg	Val	His	Tyr	Tyr	Val	Phe	Thr	Asp	Gln	Pro	Ala	Ala	Val	Pro		
145				150						155					160		
Arg	Val	Thr	Leu	Gly	Thr	Gly	Arg	Gln	Leu	Ser	Val	Leu	Glu	Val	Gly		
			165						170					175			
Ala	Tyr	Lys	Arg	Trp	Gln	Asp	Val	Ser	Met	Arg	Arg	Met	Glu	Met	Ile		
		180						185					190				
Ser	Asp	Phe	Cys	Glu	Arg	Arg	Phe	Leu	Ser	Glu	Val	Asp	Tyr	Leu	Val		
		195					200					205					

Cys Val Asp Val Asp Met Glu Phe Arg Asp His Val Gly Val Glu Ile
210 215 220

Leu Thr Pro Leu Phe Gly Thr Leu His Pro Ser Phe Tyr Gly Ser Ser
225 230 235 240

Arg Glu Ala Phe Thr Tyr Glu Arg Arg Pro Gln Ser Gln Ala Tyr Ile
245 250 255

Pro Lys Asp Glu Gly Asp Phe Tyr Tyr Met Gly Ala Phe Phe Gly Gly
260 265 270

Ser Val Gln Glu Val Gln Arg Leu Thr Arg Ala Cys His Gln Ala Met
275 280 285

Met Val Asp Gln Ala Asn Gly Ile Glu Ala Val Trp His Asp Glu Ser
290 295 300

His Leu Asn Lys Tyr Leu Leu Arg His Lys Pro Thr Lys Val Leu Ser
305 310 315 320

Pro Glu Tyr Leu Trp Asp Gln Gln Leu Leu Gly Trp Pro Ala Val Leu
325 330 335

Arg Lys Leu Arg Phe Thr Ala Val Pro Lys Asn His Gln Ala Val Arg
340 345 350

Asn Pro

<210> 14
<211> 23
<212> DNA
<213> Artificial

<400> 14

ggcctgtact acatttgcct gga 23

<210> 15
<211> 26
<212> DNA
<213> Artificial

<400> 15

gaaatagtgt caagtttcca tcacaa 26

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cgatgtggct gcggagccac cggcaggtaa tcctgttgat gctgattgtc tcaac 55

<210> 17
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<212> PRT
<213> Mus musculus

<400> 17

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Arg Ser Lys Ser Glu Thr Ser Leu Pro Ser Ser Arg Ser Gly Ser Gln
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Glu Lys Ile Met Asn Val Lys Gly Lys Val Ile Leu Leu Met Leu Ile
35 40 45

Val Ser
50

<210> 18
<211> 17
<212> PRT
<213> Artificial

<400> 18

Met Trp Leu Arg Ser His Arg Gln Val Ile Leu Leu Met Leu Ile Val
1 5 10 15

Ser

<210> 19
<211> 17
<212> PRT
<213> Artificial

<400> 19

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1 5 10 15

Ser

<210> 20
<211> 15
<212> PRT
<213> Sus scrofa

<400> 20

Met Asn Val Lys Gly Arg Val Val Leu Ser Met Leu Leu Val Ser
1 5 10 15